



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/787,267
Source: IFW0
Date Processed by STIC: 7/20/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 101787267
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO: X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 03/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/787,267

DATE: 07/20/2004

TIME: 11:34:22

Input Set : A:\GC687-3-D1-seqlist.txt

Output Set: N:\CRF4\07202004\J787267.raw

4 <110> APPLICANT: Dartois, Veronique A.
 5 Hoch, James A.
 6 Valle, Fernando
 7 Kumar, Manoj
 9 <120> TITLE OF INVENTION: 2,5-DKG Permeases
 12 <130> FILE REFERENCE: GC687-3-D1
 14 <140> CURRENT APPLICATION NUMBER: US 10/787,267
 15 <141> CURRENT FILING DATE: 2004-02-25
 17 <150> PRIOR APPLICATION NUMBER: US 09/922,501
 18 <151> PRIOR FILING DATE: 2001-08-03
 20 <150> PRIOR APPLICATION NUMBER: US 60/325,774
 21 <151> PRIOR FILING DATE: 2000-08-04
 23 <150> PRIOR APPLICATION NUMBER: US 60/421,141
 24 <151> PRIOR FILING DATE: 2000-09-29
 26 <160> NUMBER OF SEQ ID NOS: 22
 28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 1500
 32 <212> TYPE: DNA
 33 <213> ORGANISM: environmental source
 35 <220> FEATURE:
 36 <221> NAME/KEY: CDS
 37 <222> LOCATION: (94)...(1374)
 39 <400> SEQUENCE: 1

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 41 gcgtcatgaa cctcaacttt agtaggcaag cct atg aac agc tct acc aat gca 114
 42 Met Asn Ser Ser Thr Asn Ala
 43 1 5
 45 acg aaa cgc tgg tgg tac atc atg cct atc gtg ttt atc acg tat agc 162
 46 Thr Lys Arg Trp Trp Tyr Ile Met Pro Ile Val Phe Ile Thr Tyr Ser
 47 10 15 20
 49 ctg gcg tat ctc gac cgc gca aac ttc agc ttt gct tcg gca gcg ggc 210
 50 Leu Ala Tyr Leu Asp Arg Ala Asn Phe Ser Phe Ala Ser Ala Ala Gly
 51 25 30 35
 53 att acg gaa gat tta ggc att acc aaa ggc atc tcg tcg ctt ctt ggc 258
 54 Ile Thr Glu Asp Leu Gly Ile Thr Lys Gly Ile Ser Ser Leu Leu Gly
 55 40 45 50 55
 57 gca ctt ttc ttc ctc ggc tat ttc ttc ttc cag atc ccg ggg gcg att 306
 58 Ala Leu Phe Phe Leu Gly Tyr Phe Phe Phe Gln Ile Pro Gly Ala Ile
 59 60 65 70
 61 tac gcg gaa cgc cgt agc gta cgg aag ctg att ttc atc tgt ctg atc 354
 62 Tyr Ala Glu Arg Arg Ser Val Arg Lys Leu Ile Phe Ile Cys Leu Ile
 63 75 80 85

mandatory, <213> has to be
 either artificial/unknown OR
 Does Not Comply genus/species
 Corrected Diskette Needed

Invalid
 Response

Please see item #10 on error
 summary sheet.

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Input Set : A:\GC687-3-D1-seqlist.txt

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65	ctg	tgg	ggc	gcc	tgc	gcc	tcg	ctt	gac	cgg	gat	ggg	gca	caa	tat	tcc	402
66	Leu	Trp	Gly	Ala	Cys	Ala	Ser	Leu	Asp	Arg	Asp	Gly	Ala	Gln	Tyr	Ser	
67		90						95					100				
69	agc	gct	ggc	tgg	cga	tcc	gtt	tta	ttc	tcg	gct	gtc	gtg	gaa	gcg	gcg	450
70	Ser	Ala	Gly	Trp	Arg	Ser	Val	Leu	Phe	Ser	Ala	Val	Val	Glu	Ala	Ala	
71		105						110					115				
73	gtc	atg	ccg	gcg	atg	ctg	att	tac	atc	agt	aac	tgg	ttt	acc	aaa	tca	498
74	Val	Met	Pro	Ala	Met	Leu	Ile	Tyr	Ile	Ser	Asn	Trp	Phe	Thr	Lys	Ser	
75	120					125					130					135	
77	gaa	cgt	tca	cg	gcc	aac	acc	ttc	tta	atc	ctc	ggc	aac	ccg	gtc	acg	546
78	Glu	Arg	Ser	Arg	Ala	Asn	Thr	Phe	Leu	Ile	Leu	Gly	Asn	Pro	Val	Thr	
79					140					145					150		
81	gta	ctg	tgg	atg	tcg	gtg	gtc	tcc	ggc	tac	ctg	att	cag	tcc	ttc	ggc	594
82	Val	Leu	Trp	Met	Ser	Val	Val	Ser	Gly	Tyr	Leu	Ile	Gln	Ser	Phe	Gly	
83				155					160					165			
85	tgg	cgt	gaa	atg	ttt	att	att	gaa	ggc	gtt	ccg	gcc	gtc	ctc	tgg	gcc	642
86	Trp	Arg	Glu	Met	Phe	Ile	Ile	Glu	Gly	Val	Pro	Ala	Val	Leu	Trp	Ala	
87		170						175					180				
89	ttc	tgc	tgg	tgg	gtg	ctg	gtc	aaa	gtt	aaa	ccg	tcg	cag	gtg	aac	tgg	690
90	Phe	Cys	Trp	Trp	Val	Leu	Val	Lys	Val	Lys	Pro	Ser	Gln	Val	Asn	Trp	
91		185					190						195				
93	ttg	tcg	gaa	aac	gag	aaa	gcc	gcg	ctg	cag	gcg	cag	ctg	gag	agc	gag	738
94	Leu	Ser	Glu	Asn	Glu	Lys	Ala	Ala	Leu	Gln	Ala	Gln	Leu	Glu	Ser	Glu	
95	200					205					210					215	
97	cag	cag	ggg	att	aaa	gcc	gtg	cgt	aac	tac	ggc	gaa	gcc	ttc	cg	tca	786
98	Gln	Gln	Gly	Ile	Lys	Ala	Val	Arg	Asn	Tyr	Gly	Glu	Ala	Phe	Arg	Ser	
99				220					225					230			
101	cg	aac	gtc	att	cta	ctg	tgc	atg	cag	tat	ttt	gcc	tgg	agt	atc	ggc	834
102	Arg	Asn	Val	Ile	Leu	Leu	Cys	Met	Gln	Tyr	Phe	Ala	Trp	Ser	Ile	Gly	
103				235					240					245			
105	gtg	tac	ggg	ttt	gtg	ctg	tgg	ttg	ccg	tca	att	att	cg	agc	ggc	ggc	882
106	Val	Tyr	Gly	Phe	Val	Leu	Trp	Leu	Pro	Ser	Ile	Ile	Arg	Ser	Gly	Gly	
107		250						255					260				
109	gtc	aat	atg	ggg	atg	gtg	gaa	gtc	ggc	tgg	ctc	tct	tcg	gtg	cct	tat	930
110	Val	Asn	Met	Gly	Met	Val	Glu	Val	Gly	Trp	Leu	Ser	Ser	Val	Pro	Tyr	
111		265					270						275				
113	ctg	gcc	gcg	act	att	gcg	atg	atc	gtc	gtc	tcc	tgg	gct	tcc	gat	aaa	978
114	Leu	Ala	Ala	Thr	Ile	Ala	Met	Ile	Val	Val	Ser	Trp	Ala	Ser	Asp	Lys	
115	280					285					290					295	
117	atg	cag	aac	cgt	aaa	ctg	ttc	gtc	tgg	ccg	ctg	ctg	ctg	att	ggc	gga	1026
118	Met	Gln	Asn	Arg	Lys	Leu	Phe	Val	Trp	Pro	Leu	Leu	Leu	Ile	Gly	Gly	
119				300						305				310			
121	ctg	gct	ttt	att	ggc	tca	tgg	gcc	gtc	ggc	gct	aac	cat	ttc	tgg	gcc	1074
122	Leu	Ala	Phe	Ile	Gly	Ser	Trp	Ala	Val	Gly	Ala	Asn	His	Phe	Trp	Ala	
123				315					320					325			
125	tct	tat	acc	ctg	ctg	gtg	att	gcc	aat	gcg	gca	atg	tac	gcc	cct	tac	1122
126	Ser	Tyr	Thr	Leu	Leu	Val	Ile	Ala	Asn	Ala	Ala	Met	Tyr	Ala	Pro	Tyr	
127		330						335					340				
129	ggg	ccg	ttt	ttc	gcc	atc	att	ccg	gaa	atg	ctg	ccg	cgt	aac	gtc	gcc	1170

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130 Gly Pro Phe Phe Ala Ile Ile Pro Glu Met Leu Pro Arg Asn Val Ala
131      345      350      355
133 ggt ggc gca atg gcg ctc atc aac agc atg ggg gcc tta ggt tca ttc      1218
134 Gly Gly Ala Met Ala Leu Ile Asn Ser Met Gly Ala Leu Gly Ser Phe
135 360      365      370      375
137 ttt ggt tgc tgg ttc gtg ggc tac ctg aac ggc acc acc ggc agt cca      1266
138 Phe Gly Ser Trp Phe Val Gly Tyr Leu Asn Gly Thr Thr Gly Ser Pro
139      380      385      390
141 tca gcc tca tac att ttc atg gga gtg gcg ctt ttc gcc tgc gta tgg      1314
142 Ser Ala Ser Tyr Ile Phe Met Gly Val Ala Leu Phe Ala Ser Val Trp
143      395      400      405
145 ctt act tta att gtt aag cct gct aac aat caa aag ctc ccc atc ggc      1362
146 Leu Thr Leu Ile Val Lys Pro Ala Asn Asn Gln Lys Leu Pro Ile Gly
147      410      415      420
149 gct cgt cac gcc tgacctttac tacttacgga gatcacgcct tgggtacgtt      1414
150 Ala Arg His Ala
151      425
153 gcaggacaaa ccgataggca ccgcaaaggc tggggccatc gagcagcgcg taaacagtca      1474
154 gctggttgct gtcgctgtgc ggcgtc      1500
156 <210> SEQ ID NO: 2
157 <211> LENGTH: 427
158 <212> TYPE: PRT
159 <213> ORGANISM: environmental source
161 <400> SEQUENCE: 2
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163 1      5      10      15
164 Ile Val Phe Ile Thr Tyr Ser Leu Ala Tyr Leu Asp Arg Ala Asn Phe
165      20      25      30
166 Ser Phe Ala Ser Ala Ala Gly Ile Thr Glu Asp Leu Gly Ile Thr Lys
167      35      40      45
168 Gly Ile Ser Ser Leu Leu Gly Ala Leu Phe Phe Leu Gly Tyr Phe Phe
169      50      55      60
170 Phe Gln Ile Pro Gly Ala Ile Tyr Ala Glu Arg Arg Ser Val Arg Lys
171 65      70      75      80
172 Leu Ile Phe Ile Cys Leu Ile Leu Trp Gly Ala Cys Ala Ser Leu Asp
173      85      90      95
174 Arg Asp Gly Ala Gln Tyr Ser Ser Ala Gly Trp Arg Ser Val Leu Phe
175      100      105      110
176 Ser Ala Val Val Glu Ala Ala Val Met Pro Ala Met Leu Ile Tyr Ile
177      115      120      125
178 Ser Asn Trp Phe Thr Lys Ser Glu Arg Ser Arg Ala Asn Thr Phe Leu
179      130      135      140
180 Ile Leu Gly Asn Pro Val Thr Val Leu Trp Met Ser Val Val Ser Gly
181 145      150      155      160
182 Tyr Leu Ile Gln Ser Phe Gly Trp Arg Glu Met Phe Ile Ile Glu Gly
183      165      170      175
184 Val Pro Ala Val Leu Trp Ala Phe Cys Trp Trp Val Leu Val Lys Val
185      180      185      190
186 Lys Pro Ser Gln Val Asn Trp Leu Ser Glu Asn Glu Lys Ala Ala Leu

```

Same error
 please see item #10
 on error
 summary
 sheet.

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187          195          200          205
188 Gln Ala Gln Leu Glu Ser Glu Gln Gln Gly Ile Lys Ala Val Arg Asn
189          210          215          220
190 Tyr Gly Glu Ala Phe Arg Ser Arg Asn Val Ile Leu Leu Cys Met Gln
191 225          230          235          240
192 Tyr Phe Ala Trp Ser Ile Gly Val Tyr Gly Phe Val Leu Trp Leu Pro
193          245          250          255
194 Ser Ile Ile Arg Ser Gly Gly Val Asn Met Gly Met Val Glu Val Gly
195          260          265          270
196 Trp Leu Ser Ser Val Pro Tyr Leu Ala Ala Thr Ile Ala Met Ile Val
197          275          280          285
198 Val Ser Trp Ala Ser Asp Lys Met Gln Asn Arg Lys Leu Phe Val Trp
199          290          295          300
200 Pro Leu Leu Leu Ile Gly Gly Leu Ala Phe Ile Gly Ser Trp Ala Val
201 305          310          315          320
202 Gly Ala Asn His Phe Trp Ala Ser Tyr Thr Leu Leu Val Ile Ala Asn
203          325          330          335
204 Ala Ala Met Tyr Ala Pro Tyr Gly Pro Phe Phe Ala Ile Ile Pro Glu
205          340          345          350
206 Met Leu Pro Arg Asn Val Ala Gly Gly Ala Met Ala Leu Ile Asn Ser
207          355          360          365
208 Met Gly Ala Leu Gly Ser Phe Phe Gly Ser Trp Phe Val Gly Tyr Leu
209          370          375          380
210 Asn Gly Thr Thr Gly Ser Pro Ser Ala Ser Tyr Ile Phe Met Gly Val
211 385          390          395          400
212 Ala Leu Phe Ala Ser Val Trp Leu Thr Leu Ile Val Lys Pro Ala Asn
213          405          410          415
214 Asn Gln Lys Leu Pro Ile Gly Ala Arg His Ala
215          420          425
217 <210> SEQ ID NO: 3
218 <211> LENGTH: 1775
219 <212> TYPE: DNA
220 <213> ORGANISM: (environmental source)
222 <220> FEATURE:
223 <221> NAME/KEY: CDS
224 <222> LOCATION: (214)...(1491)
226 <400> SEQUENCE: 3
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228 cctgcgctat tcgcaaagtg gtggtgaaaa taccgctgcg ttatttaacg cccaataagc 120
229 aacaccgagt ttataaccct gaacgacacg gctgcgggcc tgtgtagacg cccctacgcc 180
230 ttaacaccac taaatgactc tacaggtgta tat atg aat aca gcc tct gtt tct 234
231 Met Asn Thr Ala Ser Val Ser
232          1          5
234 gtc acc caa agc cag gcg atc ccc aaa tta cgc tgg ttg aga ata gtg 282
235 Val Thr Gln Ser Gln Ala Ile Pro Lys Leu Arg Trp Leu Arg Ile Val
236          10          15          20
238 ccg cct att ctt att acc tgc att att tcc tat atg gac cgg gtg aac 330
239 Pro Pro Ile Leu Ile Thr Cys Ile Ile Ser Tyr Met Asp Arg Val Asn
240          25          30          35

```

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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Input Set : A:\GC687-3-D1-seqlist.txt

Output Set: N:\CRF4\07202004\J787267.raw

242	atc	gcc	ttc	gcc	atg	ccc	ggc	ggc	atg	gac	gat	gaa	ctg	ggc	atc	acc	378
243	Ile	Ala	Phe	Ala	Met	Pro	Gly	Gly	Met	Asp	Asp	Glu	Leu	Gly	Ile	Thr	
244	40					45				50						55	
246	gcc	tcg	atg	gcc	ggg	ttg	gcc	ggc	ggt	att	ttc	ttt	atc	ggt	tat	ctg	426
247	Ala	Ser	Met	Ala	Gly	Leu	Ala	Gly	Gly	Ile	Phe	Phe	Ile	Gly	Tyr	Leu	
248					60					65					70		
250	ttc	ttg	cag	gta	ccc	ggc	ggc	aag	ctg	gcg	gtg	tac	ggc	aac	ggc	aag	474
251	Phe	Leu	Gln	Val	Pro	Gly	Gly	Lys	Leu	Ala	Val	Tyr	Gly	Asn	Gly	Lys	
252					75				80					85			
254	aaa	ttc	atc	ggt	tgg	tcg	ttg	ttg	gcc	tgg	gcg	gtg	att	tcc	gtg	ctg	522
255	Lys	Phe	Ile	Gly	Trp	Ser	Leu	Leu	Ala	Trp	Ala	Val	Ile	Ser	Val	Leu	
256			90						95				100				
258	acc	ggg	ctg	gtc	acg	aat	cag	tat	caa	ttg	ctg	ttc	ctg	cgc	ttc	gcc	570
259	Thr	Gly	Leu	Val	Thr	Asn	Gln	Tyr	Gln	Leu	Leu	Phe	Leu	Arg	Phe	Ala	
260			105					110				115					
262	ctc	ggc	cgt	ttc	cga	agc	ggc	atg	ctg	cgg	tgg	gtg	ctg	acc	atg	atc	618
263	Leu	Gly	Arg	Phe	Arg	Ser	Gly	Met	Leu	Arg	Trp	Val	Leu	Thr	Met	Ile	
264	120					125					130				135		
266	agc	aac	tgg	ttc	ccg	gac	aag	gaa	cgc	ggg	cgc	gcc	aac	gcc	atc	gtc	666
267	Ser	Asn	Trp	Phe	Pro	Asp	Lys	Glu	Arg	Gly	Arg	Ala	Asn	Ala	Ile	Val	
268					140					145					150		
270	atc	atg	ttc	gtg	ccg	atc	gcc	ggc	atc	ctt	acc	gca	ccg	ctg	tcc	ggc	714
271	Ile	Met	Phe	Val	Pro	Ile	Ala	Gly	Ile	Leu	Thr	Ala	Pro	Leu	Ser	Gly	
272				155					160						165		
274	tgg	atc	atc	acc	gcc	tgg	gac	tgg	cgc	atg	ctg	ttc	ctg	gtc	gag	ggc	762
275	Trp	Ile	Ile	Thr	Ala	Trp	Asp	Trp	Arg	Met	Leu	Phe	Leu	Val	Glu	Gly	
276			170					175				180					
278	gcg	ctg	tcg	ctg	gtc	gtg	atg	gtg	ctg	tgg	tat	ttc	acc	atc	agc	aac	810
279	Ala	Leu	Ser	Leu	Val	Val	Met	Val	Leu	Trp	Tyr	Phe	Thr	Ile	Ser	Asn	
280			185				190				195						
282	cgt	cca	caa	gag	gcc	aaa	agg	att	tcg	cag	gcg	gaa	aaa	gat	tat	ctg	858
283	Arg	Pro	Gln	Glu	Ala	Lys	Arg	Ile	Ser	Gln	Ala	Glu	Lys	Asp	Tyr	Leu	
284	200					205					210				215		
286	atc	aaa	acg	ctg	cac	gac	gaa	cag	ttg	ctg	atc	aaa	ggc	aaa	acg	gtg	906
287	Ile	Lys	Thr	Leu	His	Asp	Glu	Gln	Leu	Leu	Ile	Lys	Gly	Lys	Thr	Val	
288					220					225					230		
290	cgc	aac	gcc	tcg	ctg	cgt	cgg	gtg	ctg	ggc	gac	aaa	atc	atg	tgg	aag	954
291	Arg	Asn	Ala	Ser	Leu	Arg	Arg	Val	Leu	Gly	Asp	Lys	Ile	Met	Trp	Lys	
292					235				240					245			
294	ttc	ttc	tac	cag	acc	ggg	ata	tac	ggc	tac	acc	ctg	tgg	ctg	ccg	acc	1002
295	Phe	Phe	Tyr	Gln	Thr	Gly	Ile	Tyr	Gly	Tyr	Thr	Leu	Trp	Leu	Pro	Thr	
296			250					255				260					
298	att	ctc	aag	ggg	ctc	acc	aac	ggc	aat	atg	gag	cag	gtc	ggg	atg	ctg	1050
299	Ile	Leu	Lys	Gly	Leu	Thr	Asn	Gly	Asn	Met	Glu	Gln	Val	Gly	Met	Leu	
300			265				270				275						
302	gct	atc	ctg	ccc	tat	atc	ggc	gcc	atc	ttc	ggc	atg	ctg	atc	att	tcc	1098
303	Ala	Ile	Leu	Pro	Tyr	Ile	Gly	Ala	Ile	Phe	Gly	Met	Leu	Ile	Ile	Ser	
304	280					285					290				295		
306	acc	ctc	tcc	gat	cgc	acc	ggc	aag	cgc	aaa	gtg	ttc	gtc	gca	ctg	ccg	1146

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/787,267

DATE: 07/20/2004

TIME: 11:34:23

Input Set : A:\GC687-3-D1-seqlist.txt

Output Set: N:\CRF4\07202004\J787267.raw

:1172 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13

:1175 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13